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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/885,188

DATE: 01/25/2002
 TIME: 17:01:04

Input Set : N:\Crf3\RULE60\09885188.raw
 Output Set: N:\CRF3\01252002\I885188.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

- 2 (i) APPLICANT: Chris Somerville
 3 Pierre Broun
 4 Frank van de Loo
 5 (ii) TITLE OF INVENTION: Production of Hydroxylated Fatty Acids in
 6 Genetically Modified Plants
 7 (iii) NUMBER OF SEQUENCES: 15
 8 (iv) CORRESPONDENCE ADDRESS:
 9 (A) ADDRESSEE: Pillsbury Winthrop, L.L.P.
 10 (B) STREET: 1600 Tysons Boulevard
 11 (C) CITY: McLean
 12 (D) STATE: VA
 13 (E) COUNTRY: USA
 14 (F) ZIP: 22102
 15 (v) COMPUTER READABLE FORM:
 16 (A) MEDIUM TYPE: Diskette, 3.50 inch
 17 (B) COMPUTER: IBM PC-compatible
 18 (C) OPERATING SYSTEM: MS-DOS
 19 (D) SOFTWARE: MS Word
 20 (vi) CURRENT APPLICATION DATA:
 C--> 21 (A) APPLICATION NUMBER: US/09/885,188
 C--> 22 (B) FILING DATE: 21-Jun-2001
 23 (C) CLASSIFICATION:
 24 (vii) PRIOR APPLICATION DATA:
 25 (A) APPLICATION NUMBER: US/08/530,862B
 26 (B) FILING DATE: 06-Feb-1996
 27 (A) APPLICATION NUMBER: PCT/US95/11855
 28 (B) FILING DATE: September 25, 1995
 29 (A) APPLICATION NUMBER: US 08/530,862
 30 (B) FILING DATE: September 20, 1995
 31 (A) APPLICATION NUMBER: US 08/320,982
 32 (B) FILING DATE: October 11, 1994
 33 (A) APPLICATION NUMBER: US 08/314,596
 34 (B) FILING DATE: September 26, 1994
 35 (2) INFORMATION FOR SEQ ID NO: 1
 36 (i) SEQUENCE CHARACTERISTICS:
 37 (A) LENGTH: 543 nucleotides
 38 (B) TYPE: nucleotide
 39 (C) STRANDEDNESS: single
 40 (D) TOPOLOGY: linear
 41 (ii) MOLECULE TYPE: cDNA
 42 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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43	TATTGGCACC GGCAGCACCA TTCCAACAAT GGATCCCTAG AAAAAAGATGA AGTCTTTGTC	60
44	CCACCTAAGA AAGCTGCAGT CANATGGTAT GTCAAATACC TCAACAACCC TCTTGGACGC	120
45	ATTCTGGTGT TAACAGTTCA GTTTATCCTC GGGTGGCCTT TGTATCTAGC CTTTAATGTA	180
46	TCAGGTAGAC CTTATGATGG TTTCGCTTCA CATTCTTCC CTCATGCACC TATCTTTAAG	240
47	GACCGTGAAC GTCTCCAGAT ATACATCTCA GATGCTGGTA TTCTAGCTGT CTGTTATGGT	300
48	CTTTACCGTT ACGCTGCTTC ACAAGGATTG ACTGCTATGA TCTGCGTCTA CGGAGTACCG	360
49	CTTTTGATAG TGAACTTTTT CCTGTCTTG GTCACCTTCT TGCAGCACAC TCATCCTTCA	420
50	TTACCTCACT ATGATTCAAC CGAGTGGGAA TGGATTAGAG GAGCTTTGGT TACGGTAGAC	480
51	AGAGACTATG GAATCTTGAA CAAGGTGTTT CACAACATAA CAGACACCCA CGTAGCACAC	540
52	CAC	543

54 (2) INFORMATION FOR SEQ ID NO: 2

55 (i) SEQUENCE CHARACTERISTICS:

56 (A) LENGTH: 544 nucleotides

57 (B) TYPE: nucleotide

58 (C) STRANDEDNESS: single

59 (D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: cDNA

61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

62	TATAGGCACC GGAGGCACCA TTCCAACACA GGATCCCTCG AAAGAGATGA AGTATTTGTC	60
63	CCAAAGCAGA AATCCGCAAT CAAGTGGTAC GGCGAATACC TCAACAACCC TCCTGGTCGC	120
64	ATCATGATGT TAACTGTCCA GTTCGTCTC GGATGGCCCT TGTACTTAGC CTTCAACGTT	180
65	TCTGGCAGAC CCTACAATGG TTTCGCTTCC CATTCTTCC CCAATGCTCC TATCTACAAC	240
66	GACCGTGAAC GCCTCCAGAT TTACATCTCT GATGCTGGTA TTCTAGCCGT CTGTTATGGT	300
67	CTTTACCGTT ACGCTGTTGC ACAAGGACTA GCCTCAATGA TCTGTCTAAA CGGAGTTCCG	360
68	CTTCTGATAG TTAACTTTTT CCTCGTCTTG ATCACTTACT TACAACACAC TCACCCTGCG	420
69	TTGCCTCACT ATGATTCATC AGAGTGGGAT TGGCTTAGAG GAGCTTTAGC TACTGTAGAC	480
70	AGAGACTATG GAATCTTGAA CAAGGTGTTC CATAACATCA CAGACACCCA CGTCGCACAC	540
71	CACT	544

73 (2) INFORMATION FOR SEQ ID NO: 3

74 (i) SEQUENCE CHARACTERISTICS:

75 (A) LENGTH: 1855 nucleotides

76 (B) TYPE: nucleotide

77 (C) STRANDEDNESS: single

78 (D) TOPOLOGY: linear

79 (ii) MOLECULE TYPE: genomic

80 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

81	ATGAAGCTTT ATAAGAAGTT AGTTTTCTCT GGTGACAGAG AAATTNTGTC AATTGGTAGT	60
82	GACAGTTGAA GCAACAGGAA CAACAAGGAT GGTTGGTGNT GATGCTGATG TGGTGATGTG	120
83	TTATTCATCA AATACTAAAT ACTACATTAC TTGTTGCTGC CTACTTCTCC TATTTCTCTC	180
84	GCCACCCATT TTGGACCCAC GANCTTCCA TTTAAACCCCT CTCTCGTGCT ATTCACCAGA	240
85	AGAGAAGCCA AGAGAGAGAG AGAGAGAATG TTCTGAGGAT CATTGTCTTC TTCATCGTTA	300
86	TTAACGTAAG TTTTTTTTGA CCACTCATAT CTAAAATCTA GTACATGCAA TAGATTAATG	360
87	ACTGTTCTTT CTTTGTATAT TTTCAGCTTC TTGAATTCAG GATGGGTGCT GGTGGAAGAA	420
88	TAATGGTTAC CCCCTCTTCC AAGAAATCAG AAAGTGAAGC CCTAAAACGT GGACCATGTG	480
89	AGAAACCACC ATTCAGTGT AAAGATCTGA AGAAAGCAAT CCCACAGCAT TGTTTCAAGC	540
90	GCTCTATCCC TCGTTCTTTC TCCTACCTTC TCACAGATAT CACTTTAGTT TCTTGCTTCT	600
91	ACTACGTTGC CACAAATTAC TTCTCTCTTC TTCCTCAGCC TCTCTCTACT TACCTAGCTT	660
92	GGCCTCTCTA TTGGGTATGT CAAGGCTGTG TCTTAACCGG TATCTGGGTC ATTGGCCATG	720
93	AATGTGGTCA CCATGCATTC AGTGACTATC AATGGGTAGA TGACACTGTT GGTTTTATCT	780

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94   TCCATTCCCTT CTTTCTCGTC CCTTACTTCT CCTGGAAATA CAGTCATCGT CGTCACCATT      840
95   CCAACAATGG ATCTCTCGAG AAAGATGAAG TCTTTGTCCC ACCGAAGAAA GCTGCAGTCA      900
96   AATGGTATGT TAAATACCTC AACAACCCTC TTGGACGCAT TCTGGTGTTA ACAGTTCAGT      960
97   TTATCCTCGG GTGGCCTTTG TATCTAGCCT TTAATGTATC AGGTAGACCT TATGATGGTT     1020
98   TCGCTTCACA TTTCTTCCCT CATGCACCTA TCTTTAAAGA CCGAGAACGC CTCCAGATAT     1080
99   ACATCTCAGA TGCTGGTATT CTAGCTGTCT GTTATGGTCT TTACCGTTAC GCTGCTTCAC     1140
100  AAGGATTGAC TGCTATGATC TGCCTCTATG GAGTACCGCT TTTGATAGTG AACTTTTTTCC     1200
101  TTGTCTTGGT AACTTTCTTG CAGCACACTC ATCCTTCGTT ACCTCATTAT GATTCAACCG     1260
102  AGTGGGAATG GATTAGAGGA GCTTTGGTTA CGGTAGACAG AGACTATGGA ATATTGAACA     1320
103  AGGTGTTCCA TAACATAACA GACACACATG TGGCTCATCA TCTCTTTGCA ACTATACCGC     1380
104  ATTATAACGC AATGGAAGCT ACAGAGGCGA TAAAGCCAAT ACTTGGTGAT TACTACCACT     1440
105  TCGATGGAAC ACCGTGGTAT GTGGCCATGT ATAGGGAAGC AAAGGAGTGT CTCTATGTAG     1500
106  AACCGGATAC GGAACGTGGG AAGAAAGGTG TCTACTATTA CAACAATAAG TTATGAGGCT     1560
107  GATAGGGCGA GAGAAGTGCA ATTATCAATC TTCATTTCCA TGTTTTAGGT GTCTTGTTTA     1620
108  AGAAGCTATG CTTTGTTTTCA ATAATCTCAG AGTCCATNTA GTTGTGTTCT GGTGCATTTT     1680
109  GCCTAGTTAT GTGGTGTCGG AAGTTAGTGT TCAAACGTCT TCCTGCTGTG CTGCCCAGTG     1740
110  AAGAACAAGT TTACGTGTTT AAAATACTCG GAACGAATTG ACCACAANAT ATCCAAAACC     1800
111  GGCTATCCGA ATTCATATAT CGAAAACCGG ATATCCAAAT TTCCAGAGTA CTTAG         1855

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113 (2) INFORMATION FOR SEQ ID NO: 4

114 (i) SEQUENCE CHARACTERISTICS:

115 (A) LENGTH: 384 amino acids

116 (B) TYPE: amino acid

117 (C) STRANDEDNESS:

118 (D) TOPOLOGY: linear

119 (ii) MOLECULE TYPE: protein

120 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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121  Met Gly Ala Gly Gly Arg Ile Met Val Thr Pro Ser Ser Lys Lys Ser
122  1          5          10          15
123  Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys Glu Lys Pro Pro Phe Thr
124  20          25          30
125  Val Lys Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Lys Arg Ser
126  35          40          45
127  Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Thr Leu Val Ser
128  50          55          60
129  Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
130  65          70          75          80
131  Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys
132  85          90          95
133  Val Leu Thr Gly Ile Trp Val Ile Gly His Glu Cys Gly His His Ala
134  100         105         110
135  Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Phe Ile Phe His
136  115         120         125
137  Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg
138  130         135         140
139  His His Ser Asn Asn Gly Ser Leu Glu Lys Asp Glu Val Phe Val Pro
140  145         150         155         160
141  Pro Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro
142  165         170         175
143  Leu Gly Arg Ile Leu Val Leu Thr Val Gln Phe Ile Leu Gly Trp Pro

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144		180		185		190
145	Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala					
146		195		200		205
147	Ser His Phe Phe Pro His Ala Pro Ile Phe Lys Asp Arg Glu Arg Leu					
148		210		215		220
149	Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu					
150		225		230		235
151	Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr Ala Met Ile Cys Val Tyr					
152		245		250		255
153	Gly Val Pro Leu Leu Ile Val Asn Phe Phe Leu Val Leu Val Thr Phe					
154		260		265		270
155	Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp					
156		275		280		285
157	Glu Trp Ile Arg Gly Ala Leu Val Thr Val Asp Arg Asp Tyr Gly Ile					
158		290		295		300
159	Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His					
160		305		310		315
161	Leu Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala					
162		325		330		335
163	Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp					
164		340		345		350
165	Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro					
166		355		360		365
167	Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu					
168		370		375		380

170 (2) INFORMATION FOR SEQ ID NO: 5

171 (i) SEQUENCE CHARACTERISTICS:

172 (A) LENGTH: 387 amino acids

173 (B) TYPE: amino acid

174 (C) STRANDEDNESS:

175 (D) TOPOLOGY: linear

176 (ii) MOLECULE TYPE: protein

177 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

178	Met Gly Gly Gly Arg Met Ser Thr Val Ile Thr Ser Asn Asn Ser
179	1 5 10 15
180	Glu Lys Lys Gly Gly Ser Ser His Leu Lys Arg Ala Pro His Thr Lys
181	20 25 30
182	Pro Pro Phe Thr Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys
183	35 40 45
184	Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val
185	50 55 60
186	Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr
187	65 70 75 80
188	Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe
189	85 90 95
190	Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly
191	100 105 110
192	His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu
193	115 120 125

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194   Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser
195       130                      135                      140
196   His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val
197   145                      150                      155                      160
198   Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Ser
199                      165                      170                      175
200   Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu
201                      180                      185                      190
202   Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
203                      195                      200                      205
204   Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg
205       210                      215                      220
206   Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr
207   225                      230                      235                      240
208   Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met
209                      245                      250                      255
210   Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met
211                      260                      265                      270
212   Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser
213       275                      280                      285
214   Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp
215       290                      295                      300
216   Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val
217   305                      310                      315                      320
218   Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala
219                      325                      330                      335
220   Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly
221                      340                      345                      350
222   Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe
223       355                      360                      365
224   Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg
225       370                      375                      380
226   Asn Lys Tyr
227       385

```

229 (2) INFORMATION FOR SEQ ID NO: 6

230 (i) SEQUENCE CHARACTERISTICS:

231 (A) LENGTH: 383 amino acids

232 (B) TYPE: amino acid

233 (C) STRANDEDNESS:

234 (D) TOPOLOGY: linear

235 (ii) MOLECULE TYPE: protein

236 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

237   Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser
238       1                      5                      10                      15
239   Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser
240                      20                      25                      30
241   Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
242       35                      40                      45
243   Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/885,188

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TIME: 17:01:06

Input Set : N:\Crf3\RULE60\09885188.raw

Output Set: N:\CRF3\01252002\I885188.raw

L:21 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:22 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]